FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
1	75	84XXX	NEW	Chemistry	Chemistry, enzyme activity	Thiopurine S-methyltransferase (TPMT)	Crosswalk to 82657: 1 Gapfill: 11 Abstain: 0
2	39	80220	Reconsideration	Chemistry	Chemistry Specimen: blood Analyte: Hydroxychloroquine Type of code: Chemistry LC-MS/MS	Hydroxychloroquine	Crosswalk to 80204: 10 Crosswalk to 80299: 2 Gapfill: 0 Abstain 0
3	41	83529	Reconsideration	Chemistry	Chemistry Specimen: blood Analyte: Interleukin 6 Type of code: Chemistry	Interleukin-6 (IL-6)	Crosswalk to 83006: 9 Crosswalk to 83520: 3 Gapfill: 0 Abstain: 0
4	96	0X46U	PLA	Chemistry	Specimen: blood (serum) Analyte: lipid extracts Indication: to determine risk for NASH Type of code: Chemistry using HPLC with high resolution MS	Hepatology (nonalcoholic fatty liver disease [NAFLD]), semiquantitative evaluation of 28 lipid markers by liquid chromatography with tandem mass spectrometry (LC-MS/MS), serum, reported as at-risk for nonalcoholic steatohepatitis (NASH) or not NASH	Gapfill: 12 Abstain: 0
5	98	0X48U	PLA	Chemistry	Specimen: plasma Analyte: Aβ40 and Aβ42 peptides Type of code: chemistry to determine amyloid beta 42/40 ratio.	Beta amyloid, Aβ40 and Aβ42 by liquid chromatography with tandem mass spectrometry (LC-MS/MS), ratio, plasma	Gapfill: 12 Abstain: 0
6	14	0298U	PLA	Genomic Sequencing Related Tests WHOLE GENOME Drug metabolism pharmacogenomics/pharmcogenetics	Oncology pan tumor therapy optimization Whole transcriptome Specimen: solid tissue, blood tissue and/or bone marrow tissue Analyte: RNA Type of code: GSP (whole trascriptome)	Oncology (pan tumor), whole transcriptome sequencing of paired malignant and normal RNA specimens, fresh or formalin-fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and expression level and chimeric transcript identification	Crosswalk to 0266U TIMES 1.5: 10 Gapfill: 2 Abstain: 0
7	13	0297U	PLA	Genomic Sequencing Related Tests WHOLE GENOME Drug metabolism pharmacogenomics/pharmcogenetics	Oncology pan tumor therapy optimization Whole genome Specimen: solid tissue, blood tissue and/or bone marrow tissue Analyte: DNA (e.g., vs. RNA) Type of code: GSP (whole genome)	Oncology (pan tumor), whole genome sequencing of paired malignant and normal DNA specimens, fresh or formalinfixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and variant identification	Crosswalk to 0265U TIMES 1.5: 10 Crosswalk to 0013U: 0 Crosswalk to 81425: 0 Gapfill: 2 Abstain: 0
8	15	0299U	PLA	Genomic Sequencing Related Tests WHOLE GENOME Drug metabolism pharmacogenomics/pharmcogeneticsts	Oncology pan tumor therapy optimization Whole genome Specimen: solid tissue, blood tissue and/or bone marrow tissue Analyte: DNA Type of code: GSP (whole genome)	Oncology (pan tumor), whole genome optical genome mapping of paired malignant and normal DNA specimens, fresh frozen tissue, blood, or bone marrow, comparative structural variant identification	Crosswalk to 0264U TIMES 1.5: 10 Gapfill: 2 Abstain: 0
9	16	0300U	PLA	Genomic Sequencing Related Tests WHOLE GENOME Drug metabolism pharmacogenomics/pharmcogeneticsts	Oncology pan tumor therapy optimization Whole genome Specimen: solid tissue, blood tissue and/or bone marrow tissue Analyte: DNA (e.g., vs. RNA)mparative analyses, optical sequence ID'tion + variations Type of code: GSP (whole genome)	Oncology (pan tumor), whole genome sequencing and optical genome mapping of paired malignant and normal DNA specimens, fresh tissue, blood, or bone marrow, comparative sequence analyses and variant identification	Crosswalk to 0267U TIMES 1.5: 10 Gapfill: 2 Abstain: 0
10	70	8X000	NEW	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Drug metabolism pharmacogenomics/pharmcogenetics Specimen: blood Analyte: DNA Indication: Used to determine CYP genetic makeup as a way to determine how the body is metabolising specific drugs based on the CYP	Drug metabolism (eg, pharmacogenomics) genomic sequence analysis panel, must include testing of at least 6 genes, including CYP2C19, CYP2D6, and CYP2D6 duplication/deletion analysis	Crosswalk to 81225 + 0070U: 1 Crosswalk to 81435 + 81436: 0 Crosswalk to 81413 + 81414: 0 Gapfill: 11 Abstain: 0
11	95	0X45U	PLA	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Drug metabolism pharmacogenomics/pharmcogenetics Specimen: blood or buccal specimen Analyte: DNA Indication: Used to determine why drug therapy is not efficacious - using pharmacogenomics to understand genomic makeup that may be	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis including reported phenotypes and impacted gene-drug interactions	Gapfill: 12 Abstain: 0
12	97	0X47U	PLA	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Drug metabolism pharmacogenomics/pharmcogenetics Specimen: buccal specimen Analyte: DNA Indication: Used to determine why drug therapy is not efficacious - using pharmacogenomics to understand genomic makeup that may be	Psychiatry (eg, depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of CYP2D6	Crosswalk to 0175U: 12 Gapfill: 0 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
13	99	0X50U	PLA	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Drug metabolism pharmacogenomics/pharmcogenetics Specimen: blood or buccal specimen Analyte: DNA Indication: Used to determine why drug therapy is not efficacious - using pharmacogenomics to understand genomic makeup that may be	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 25 gene report, with variant analysis and reported phenotypes	Gapfill: 12 Abstain: 0
14	100	0X51U	PLA	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Drug metabolism pharmacogenomics/pharmcogenetics Specimen: blood or buccal specimen Analyte: DNA Indication: Used to determine why drug therapy is not efficacious - using pharmacogenomics to understand genomic makeup that may be	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 16 gene report, with variant analysis and reported phenotypes	Crosswalk to 0175U: 12 Gapfill: 0 Abstain: 0
15	101	0X52U	PLA	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Drug metabolism pharmacogenomics/pharmcogenetics Specimen: blood or buccal specimen Analyte: DNA Indication: Used to determine why drug therapy is not efficacious - using pharmacogenomics to understand genomic makeup that may be	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis and reported phenotypes	Crosswalk to 0175U: 4 Gapfill: 8 Abstain: 0
16	2	0286U	PLA	Genomic Sequencing Related Tests TARGETED Drug metabolism pharmacogenomics/pharmcogenetics	Oncology ALL pharmacodynamics, drug metabolism gene analysis Specimen: blood Analyte: DNA Type of code: Targeted genomic sequencing	CEP72 (centrosomal protein, 72-KDa), NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (eg, drug metabolism) gene analysis, common variants	Gapfill: 12 Abstain: 0
17	67	0331U	PLA	Genomic Sequencing Related Tests WHOLE GENOME	Oncology hematolymphoid WHOLE GENOME Specimen: blood or Bone marrow Analyte: DNA Indication: optical genome mapping Type of code: Genome mapping, copy number variants,	Oncology (hematolymphoid neoplasia), optical genome mapping for copy number alterations and gene rearrangements utilizing DNA from blood or bone marrow, report of clinically significant alternations	Crosswalk to 81229: 12 Gapfill: 0 Abstain: 0
18	88	0X38U	PLA	Genomic Sequencing Related Tests WHOLE GENOME	Rare diseases Specimen: blood or saliva Analyte: DNA Indication: Parent testing to identify fetal constitutional/ heritable genomic changes (0x36U)	Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (STR) gene expansions, blood or saliva,	Crosswalk to 0215U: 12 Gapfill: 0 Abstain: 0
19	86	0X36U	PLA	Genomic Sequencing Related Tests WHOLE GENOME	Rare diseases (constitutional/heritable disorders) Specimen: amniotic Analyte: DNA Indication: Fetal testing to identify constitutional/ heritable genomic changes	Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (STR) gene expansions, fetal sample,	Crosswalk to 0214U: 12 Gapfill: 0 Abstain: 0
20	91	0X41U *Code has Advanced Diagnostic Laboratory Test (ADLT) status	PLA	Genomic Sequencing Related Tests WHOLE GENOME	Oncology pan-cancer Specimen: blood + tumor tissue Analyte: DNA (cell free from blood + whole genome sequencing of tumor tissue) Indication: pt s/p surgical treatment for cancer with phys now checking for minimal residual disease Type of code: NGS	Oncology (pan-cancer), analysis of minimal residual disease (MRD) from plasma, with assays personalized to each patient based on prior next-generation sequencing of the patient's tumor and germline DNA, reported as absence or presence of MRD, with disease-burden correlation, if appropriate	Gapfill: 12 Abstain: 0 *Code has Advanced Diagnostic Laboratory Test (ADLT) status
21	22	0306U	PLA	Genomic Sequencing Related Tests TARGETED; cf DNA	Oncology solid organ targeted Specimen: cell free Analyte: DNA Indication: baseline panel FOR FUTURE MRD comparison/activity surveillance	Oncology (minimal residual disease [MRD]), next-generation targeted sequencing analysis, cell-free DNA, initial (baseline) assessment to determine a patient-specific panel for future comparisons to evaluate for MRD (Do not report 0306U in conjunction with 0307U)	Gapfill: 12 Abstain: 0
22	23	0307U	PLA	Genomic Sequencing Related Tests TARGETED; cf DNA	Oncology solid organ targeted Specimen: cell free Analyte: DNA Indication: subsequent assessment w comparison to previously analyzed pt speciments (?0306u?)	Oncology (minimal residual disease [MRD]), next-generation targeted sequencing analysis of a patient-specific panel, cell-free DNA, subsequent assessment with comparison to previously analyzed patient specimens to evaluate for MRD (Do not report 0307U in conjunction with 0306U)	Gapfill: 12 Abstain: 0
23	34	0318U	PLA	Genomic Sequencing Related Tests TARGETED METHYLATION ANALYSIS	Congenital disorders Specimen: blood Analyte: DNA Indication: to assess for congenital epigenetic disorder(s) and methylation abnormalities	Pediatrics (congenital epigenetic disorders), whole genome methylation analysis by microarray for 50 or more genes, blood	Gapfill: 12 Abstain: 0
24	57	0229U	Reconsideration / Substantially Revised	Genomic Sequencing Related Tests TARGETED METHYLATION ANALYSIS	Oncology solid organ targeted Specimen: plasma Analyte: DNA Indication: Determine Residual Disease post definitive treatment Type of code: GSP targeted gene + promoter methylation analysis	BCAT1 (Branched chain amino acid transaminase 1) **and** IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis	Crosswalk to 81327 x 2: 11 Crosswalk to 81327: 1 Gapfill: 0 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
25	40	81349	Reconsideration	Genomic Sequencing Related Tests TARGETED CHROMOSOME	Constitutional Chromosomal abnormalities Specimen: blood Analyte: DNA Indication: Full chromosomal interrogation to identify genomic regions with normal and abnormal copy numbers	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis	Crosswalk to 81229 x 2: 1 Crosswalk to 81229: 11 Gapfill: 0 Abstain: 0
26	92	0X42U	PLA	Genomic Sequencing Related Tests TARGETED CHROMOSOME	Chromosome Specimen: blood maternal Analyte: fetal trophoblasts Indication: for abnormal chromosomes and fetal genetic makeup Type of code: whole genome sequencing and aneuploidy analses	Fetal aneuploidy DNA sequencing comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplication, mosaicism, and segmental aneuploid	Gapfill: 11 Abstain: 1
27	71	814XX	NEW	Genomic Sequencing Related Tests TARGETED	Inherited Disease Targeted Specimen: bone marrow Analyte: DNA ≥ 30 genes Indication: To assess bone marrow failure Type of code: sequence analysis panel using massively parallel DNA	Inherited bone marrow failure syndromes (IBMFS) (eg, Fanconi anemia, dyskeratosis congenita, Diamond-Blackfan anemia, Shwachman-Diamond syndrome, GATA2 deficiency syndrome, congenital amegakaryocytic thrombocytopenia) sequence analysis panel, must include sequencing of at least 30 genes, including BRCA2, BRIP1, DKC1, FANCA, FANCB,	Crosswalk to 81443: 12 Gapfill: 0 Abstain: 0
28	85	0X35U	PLA	Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS, MICROSATELLITE	Oncology solid organ Targeted Specimen: solid tissue Analyte: DNA Indication: analyses of tumor content sequence variants, rearrangements, microsatellite instability, mutation burden	Oncology (solid organ), targeted genomic sequence analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, DNA analysis, 84 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden	Crosswalk to 0244U: 11 Gapfill: 1
29	82	0276U	Revision	Genomic Sequencing Related Tests TARGETED	Hematology inherited panel Specimen: blood, buccal swab, amniotic fluid Analyte: DNA Indication: Pt with severe thrombocytopenia requiring platelet transfusions and without response to IVIG's and no family history of	Hematology (inherited thrombocytopenia), genomic sequence analysis of 42 genes, blood, buccal swab, or amniotic fluid	Crosswalk to 81443: 12 Gapfill: 0 Abstain: 0
30	69	0022U	Reconsideration	Genomic Sequencing Related Tests TARGETED VARIANTS; DNA and RNA	Oncology solid organ targeted Specimen: solid tissue Analyte: DNA and RNA Indication: analyses of tumor content sequence variants and rearrangements to inform therapy options	Targeted genomic sequence analysis panel, cholangiocarcinoma and non-small cell lung neoplasia, DNA and RNA analysis, 1-23 genes, interrogation for sequence variants and rearrangements, reported as presence/absence of variants and associated therapy(ies) to consider	Crosswalk to 0022U: 12 Gapfill: 0 Abstain: 0
31	72	814X1	NEW	Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS	Oncology solid organ Targeted Specimen: solid tissue tumor Analyte: RNA Indication: analyses of RNA tumor content sequence variants and rearrangements to determine specific genes known to be important in	Targeted genomic sequence analysis panel, solid organ neoplasm, 5-50 genes (eg, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, NRAS, MET, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed; RNA analysis	Crosswalk to 81445: 12 Gapfill: 0 Abstain: 0
32	76	81445	NEW	Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS	Oncology solid organ Targeted Specimen: solid tissue Analyte: DNA and RNA Indication: analyses of tumor DNA and RNA content sequence variants and rearrangements to inform therapy options	Targeted genomic sequence analysis panel, solid organ neoplasm, 5-50 genes (eg, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, NRAS, MET, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed; DNA analysis or combined DNA and RNA analysis	Crosswalk to 81445: 12 Gapfill: 0 Abstain: 0
33	74	814X3	NEW	Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS, ISOFORM; RNA;	Oncology solid organ Targeted Specimen: solid tissue Analyte: RNA Indication: analyses of RNA tumor content sequence variants and rearrangements	Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NPM1, NRAS, MET, NOTCH1, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy	Crosswalk to 81455: 12 Gapfill: 0 Abstain: 0
34	62	0326U	PLA	Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS, MICORSATELLITE	Oncology solid organ targeted Specimen: blood Analyte: cell free DNA Indication: interrogation for sequence variants, gene rearrangements, tumor mutational burden	Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 83 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden	Crosswalk to 0242U: 12 Gapfill: 0 Abstain: 0
35	73	814X2	NEW	Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS, ISOFORM EXPRESSION	Oncology hematolypmphoid panel Specimen: Analyte: RNA Type of code: GSP	Targeted genomic sequence analysis panel, hematolymphoid neoplasm or disorder, 5-50 genes (eg, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KRAS, KIT, MLL, NRAS, NPM1, NOTCH1), interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis	Crosswalk to 81450: 12 Gapfill: 0 Abstain: 0
36	90	0X40U	PLA	Genomic Sequencing Related Tests TARGETED; mRNA	Oncology prostate Specimen: urine Analyte: mRNA Indication: abnormal prostate specific antigen test with urine specimen to evaluate risk for prostate cancer.	Oncology (prostate), mRNA expression profiling of HOXC6 and DLX1, reverse transcription polymerase chain reaction (RT-PCR), first-void urine following digital rectal examination, algorithm reported as probability of high-grade cancer	Crosswalk to 0005U: 12 Gapfill: 0 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
37	32	0316U	PLA	Microbiology	Microbiology Specimen: urine Analyte: single protein, OspA Type of code: Diagnostic test for Borrelia burgdorferi	Borrelia burgdorferi (Lyme disease), OspA protein evaluation, urine	Crosswalk to 87449 + 87015: 12 Gapfill: 0 Abstain: 0
38	77	862XX 8X002	NEW	Microbiology	Specimen: Analyte: single protein Type of test: Immunoassay microbial identification	Hepatitis B surface antigen (HBsAg), quantitative	Crosswalk to 86316: 3 Crosswalk to 84702: 8 Gapfill: 1 Abstain: 0
39	68	87913 879X1	NEW	Microbiology	Microbiology SINGLE GENOMIC IDENTIFICATION Specimen: ?nasal? Analyte: DNA or RNA Type of code: viral genomic analysis	Infectious agent genotype analysis by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (coronavirus disease [COVID-19]), mutation identification in targeted region(s)	Crosswalk to 87910: 12 Gapfill: 0 Abstain: 0
40	78	87X68 8X009	NEW	Microbiology	Microbiology SINGLE GENOMIC IDENTIFICATION Specimen: Analyte: microbial genome Type of test: microbe genomic testing	Infectious agent detection by nucleic acid (DNA or RNA); Anaplasma phagocytophilum, amplified probe technique	Crosswalk to 87476: 12 Gapfill: 0 Abstain: 0
41	79	87X70 8X010	NEW	Microbiology	Microbiology SINGLE GENOMIC IDENTIFICATION Specimen: Analyte: microbial genome Type of test: microbe genomic testing	Infectious agent detection by nucleic acid (DNA or RNA); Babesia microti, amplified probe technique	Crosswalk to 87476: 12 Gapfill: 0 Abstain: 0
42	80	87X77 8X011	NEW	Microbiology	Microbiology SINGLE GENOMIC IDENTIFICATION Specimen: Analyte: microbial genome Type of test: microbe genomic testing	Infectious agent detection by nucleic acid (DNA or RNA); Borrelia miyamotoi, amplified probe technique	Crosswalk to 87476: 12 Gapfill: 0 Abstain: 0
43	81	87X99 8X012	NEW	Microbiology	Specimen: Analyte: microbial genome Type of test: microbe genomic testing	Infectious agent detection by nucleic acid (DNA or RNA); Ehrlichia chaffeensis, amplified probe technique	Crosswalk to 87476: 12 Gapfill: 0 Abstain: 0
44	27	0311U	PLA	Microbiology	Microbiology MIC Specimen: blood culture Analyte: ?blood cells? Indication: Bacterial MIC Type of code: MORPHOKINETIC CELLULAR ANALYSIS	Infectious disease (bacterial), quantitative antimicrobial susceptibility reported as phenotypic minimum inhibitory concentration (MIC)–based antimicrobial susceptibility for each organism identified (Do not report 0311U in conjunction with 87076, 87077, 0086U)	Gapfill: 11 Abstain: 1
45	17	0301U	PLA	Microbiology	Microbiology PANEL GENOMIC IDENTIFICATION Specimen: blood Analyte: DNA analyses of Bartonella henselae and B. quintana detection Type of test: microbe genomic analysis using droplet digital PCR	Infectious agent detection by nucleic acid (DNA or RNA), Bartonella henselae and Bartonella quintana, droplet digital PCR (ddPCR);	Crosswalk to 87471: 4 Crosswalk to 87472: 0 Gapfill: 8 Abstain: 0
46	18	0302U	PLA	Microbiology	Microbiology PANEL GENOMIC IDENTIFICATION Specimen: blood Analyte: DNA analyses of Bartonella henselae and B. quintana detection Type of test: microbe genomic analysis using droplet digital PCR and pre and post BAPGM™ liquid sample enrichment	Infectious agent detection by nucleic acid (DNA or RNA), Bartonella henselae and Bartonella quintana, droplet digital PCR (ddPCR); following liquid enrichment	Crosswalk to 87471: 3 Crosswalk to 87472: 0 Gapfill: 8 Abstain: 1
47	37	0321U	PLA	Microbiology	Microbiology PANEL GENOMIC IDENTIFICATION Specimen: urine Analyte: DNA or RNA detection Type of test: bacterial and fungal identification and MIC	Infectious agent detection by nucleic acid (DNA or RNA), genitourinary pathogens, identification of 20 bacterial and fungal organisms and identification of 16 associated antibiotic-resistance genes, multiplex amplified probe technique	Crosswalk to 87633 + 87632: 11 Gapfill: 1 Abstain: 0
48	59	0323U	PLA	Microbiology	Microbiology PANEL GENOMIC IDENTIFICATION Specimen: CSF Analyte: Baterial, Viral, Fungal or Parasitic DNA and RNA Type of code: microbiologic DNA and RNA content	Infectious agent detection by nucleic acid (DNA and RNA), central nervous system pathogen, metagenomic next-generation sequencing, cerebrospinal fluid (CSF), identification of pathogenic bacteria, viruses, parasites or fungi	Crosswalk to 0152U: 8 Gapfill: 3 Abstain: 1

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
49	66	0330U	PLA	Microbiology	Obstetric PANEL GENOMIC IDENTIFICATION Specimen: vaginal Analyte: DNA or RNA Type of code: diagnostic identification of vaginal microbial pathogens.	Infectious agent detection by nucleic acid (DNA or RNA), vaginal pathogen panel, identification of 27 organisms, amplified probe technique, vaginal swab	Crosswalk to 87633: 12 Gapfill: 0 Abstain: 0
50	103	0X54U	PLA	Microbiology	Obstetric PANEL GENOMIC IDENTIFICATION Specimen: vaginal Analyte: DNA or RNA bacterial and fungal Type of code: diagnostic identification of vaginal microbial pathogens.	Infectious disease (bacterial vaginosis and vaginitis), multiplex amplified probe technique, for detection of bacterial vaginosis–associated bacteria (BVAB-2, Atopobium vaginae, and Megasphera type 1), algorithm reported as detected or not detected and separate detection of Candida species (C. albicans, C. tropicalis, C. parapsilosis, C. dubliniensis), Candida	Crosswalk to 87631: 11 Gapfill: 0 Abstain: 1
51	104	0X55U	PLA	Microbiology	Obstetric PANEL GENOMIC IDENTIFICATION Specimen: not specified Analyte: DNA N. gonorrhoease and C. trachomatis Type of code: diagnostic identification of vaginal microbial pathogens.	Infectious agent detection by nucleic acid (DNA), Chlamydia trachomatis and Neisseria gonorrhoeae, multiplex amplified probe technique, urine, vaginal, pharyngeal, or rectal, each pathogen reported as detected or not detected	Crosswalk to 87491 + 87591: 11 Gapfill: 0 Abstain: 1
52	19	0303U	PLA	Hematology and Coagulation	Hematology, Sickle Cell nocturnal hypoxia Functional assessment, adhesion index	Hematology, red blood cell (RBC) adhesion to endothelial/subendothelial adhesion molecules, functional assessment, whole blood, with algorithmic analysis and result reported as an RBC adhesion index; hypoxic	Gapfill: 12 Abstain: 0
53	20	0304U	PLA	Hematology and Coagulation	Hematology, Sickle Cell normoxic Functional assessment RBC index	Hematology, red blood cell (RBC) adhesion to endothelial/subendothelial adhesion molecules, functional assessment, whole blood, with algorithmic analysis and result reported as an RBC adhesion index; normoxic	Gapfill: 12 Abstain: 0
54	21	0305U	PLA	Hematology and Coagulation	Hematology, Sickle Cell therapy optimization Functional assessment RBC index,	Hematology, red blood cell (RBC) functionality and deformity as a function of shear stress, whole blood, reported as a maximum elongation index	Gapfill: 12 Abstain: 0
55	1	0285U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology radiation toxicity Specimen: blood Analyte: cell free DNA Indication: Patients receiving radiation therapy for cancer where physicians would like to know if radiation toxicity is occurring.	Oncology, response to radiation, cell-free DNA, quantitative branched chain DNA amplification, plasma, reported as a radiation toxicity score	Crosswalk to 81595: 0 Crosswalk to 0118U: 0 Gapfill: 12 Abstain: 0
56	3	0287U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology thyroid recurrence Specimen: FNA or FFPE cancer tissue Analyte: DNA and mRNA Indication: When diagnosed with Bethesda Class VI thyroid cancer 0287U predicts risk of cancer recurrence required for selecting the extent	Oncology (thyroid), DNA and mRNA, next generation sequencing analysis of 112 genes, fine needle aspirate or formalinfixed paraffin-embedded (FFPE) tissue, algorithmic prediction of cancer recurrence, reported as a categorical risk result (low, intermediate, high)	Crosswalk to 0026U: 12 Gapfill: 0 Abstain: 0
57	4	0288U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology thyroid recurrence Specimen: FNA or FFPE cancer tissue Analyte: DNA and mRNA Indication: When diagnosed with Bethesda Class VI thyroid cancer 0287U predicts risk of cancer recurrence required for selecting the extent	Oncology (lung), mRNA, quantitative PCR analysis of 11 genes (BAG1, BRCA1, CDC6, CDK2AP1, ERBB3, FUT3, IL11, LCK, RND3, SH3BGR, WNT3A) and 3 reference genes (ESD, TBP, YAP1), formalin-fixed paraffin-embedded (FFPE) tumor tissue, algorithmic interpretation reported as a recurrence risk score	Crosswalk to 81522: 12 Gapfill: 0 Abstain: 0
58	5	0289U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Neurology Alzheimer risk medication optimization Specimen: blood Analyte: mRNA Type of code: Genomic sequence gene expression profile of 24 genes associated w Alzheimer's disease w algorithmic predictive risk for	Neurology (Alzheimer disease), mRNA, gene expression profiling by RNA sequencing of 24 genes, whole blood, algorithm reported as predictive risk score	Crosswalk to 0239U: 1 Crosswalk to 0203U: 6 Gapfill: 5 Abstain: 0
59	6	0290U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Neurology pain management Specimen: blood Analyte: mRNA Type of code: Genomic sequence gene expression profile of 36 genes associated w pain w algorithmic predictive risk for pain intensity	Pain management, mRNA, gene expression profiling by RNA sequencing of 36 genes, whole blood, algorithm reported as predictive risk score	Crosswalk to 0239U: 0 Crosswalk to 0203U: 6 Gapfill: 6 Abstain: 0
60	7	0291U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Psychiatry mood disorders assessment Specimen: blood Analyte: mRNA Type of code: Genomic sequence gene expression profile of 144 genes associated w mood disorders	Psychiatry (mood disorders), mRNA, gene expression profiling by RNA sequencing of 144 genes, whole blood, algorithm reported as predictive risk score	Crosswalk to 0239U: 0 Crosswalk to 0258U: 2 Gapfill: 10 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
61	8	0292U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Psychiatry PTSD stress risk Specimen: blood Analyte: mRNA Type of code: Genomic sequence gene expression profile of 72 genes associated w PTSD	Psychiatry (stress disorders), mRNA, gene expression profiling by RNA sequencing of 72 genes, whole blood, algorithm reported as predictive risk score	Crosswalk to 0239U: 0 Crosswalk to 0258U: 1 Gapfill: 11 Abstain: 0
62	9	0293U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Psychiatry suicidal risk Specimen: blood Analyte: mRNA Type of code: Genomic sequence gene expression profile of 54 genes associated w suicide	Psychiatry (suicidal ideation), mRNA, gene expression profiling by RNA sequencing of 54 genes, whole blood, algorithm reported as predictive risk score	Crosswalk to 0239U: 0 Crosswalk to 0258U: 1 Gapfill: 11 Abstain: 0
63	10	0294U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Mortality Specimen: blood Analyte: mRNA Type of code: Genomic sequence gene expression profile of 18 genes associated w longevity and mortality	Longevity and mortality risk, mRNA, gene expression profiling by RNA sequencing of 18 genes, whole blood, algorithm reported as predictive risk score	Crosswalk to 0239U: 0 Crosswwalk to 0175U: 2 Gapfill: 10 Abstain: 0
64	11	0295U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology breast recurrence Specimen: tumor tissue Analyte: 7 specified proteins Type of code: Protein expression analysis w algorithmic prediction for recurrence	Oncology (breast ductal carcinoma in situ), protein expression profiling by immunohistochemistry of 7 proteins (COX2, FOXA1, HER2, Ki-67, p16, PR, SIAH2), with 4 clinicopathologic factors (size, age, margin status, palpability), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a recurrence risk score	Crosswalk to 0045U: 0 Crosswalk to 0067U: 10 Gapfill: 2 Abstain: 0
65	24	0308U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Chemistry protein analyses Analyte: proteins Indication: Coronary artery disease Type of code: biochemical assays	Cardiology (coronary artery disease [CAD]), analysis of 3 proteins (high sensitivity [hs] troponin, adiponectin, and kidney injury molecule-1 [KIM-1]), plasma, algorithm reported as a risk score for obstructive CAD	Crosswalk to 0105U: 1 Crosswalk to 81506: 10 Gapfill: 1 Abstain: 0
66	65	0329U	PLA	Genomic Sequencing Related Tests TARGETED EXOME TRANSCRIPTOME, VARIANTS, REARRANGEMENTS,	Chemistry protein analyses Analyte: proteins Indication: Coronary artery disease Type of code: biochemical assays	Oncology (neoplasia), exome and transcriptome sequence analysis for sequence variants, gene copy number amplifications and deletions, gene rearrangements, microsatellite instability and tumor mutational burden utilizing DNA and RNA from tumor with DNA from normal blood or saliva for subtraction, report of clinically significant mutation(s) with therapy	Crosswalk to 0036U: 5 Gapfill: 7 Abstain: 0
67	25	0309U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Chemistry protein analyses Analyte: proteins Indication: Coronary artery disease Type of code: biochemical assays	Cardiology (cardiovascular disease), analysis of 4 proteins (NT-proBNP, osteopontin, tissue inhibitor of metalloproteinase-1 [TIMP-1], and kidney injury molecule-1 [KIM-1]), plasma, algorithm reported as a risk score for major adverse cardiac event	Crosswalk to 0105U: 1 Crosswalk to 81506: 9 Gapfill: 2 Abstain: 0
68	26	0310U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Chemistry protein analyses Analyte: proteins Indication: Vasculitis, Cardiac disease Type of code: biochemical assays	Pediatrics (vasculitis, Kawasaki disease [KD]), analysis of 3 biomarkers (NTproBNP, C-reactive protein, and T-uptake), plasma, algorithm reported as a risk score for KD	Crosswalk to 0105U: 0 Crosswalk to 81506: 11 Gapfill: 1 Abstain: 0
69	63	0327U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Chromosomal abnormalities, aneuploidy Specimen: maternal blood Analyte: cell free DNA Indication: 0327U is a prenatal test identifies pregnancies at risk for trisomy 21, trisomy 18, and trisomy 13, only.	Fetal aneuploidy (trisomy 13, 18, and 21), DNA sequence analysis of selected regions using maternal plasma, algorithm reported as a risk score for each trisomy, includes sex reporting, if performed	Crosswalk to 81420: 0 Crosswalk to 81507: 12 Gapfill: 0 Abstain: 0
70	33	0317U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology lung risk Specimen: blood Analyte: FISH probe for chromosome 3 deletions: 3q29, 3p22.1, 10q22.3, 10cen Type of code: Genomic sequence analysis w algorithmic analyses to	Oncology (lung cancer), four-probe FISH (3q29, 3p22.1, 10q22.3, 10cen) assay, whole blood, predictive algorithm generated evaluation reported as decreased or increased risk for lung cancer	Crosswalk to 0053U: 1 Gapfill: 11 Abstain: 0
71	35	0319U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Transplant renal early acute rejection Specimen: PRE-transplant blood Analyte: RNA expression by SELECT transcriptome Type of code: RNA/transcriptome expression	Nephrology (renal transplant), RNA expression by select transcriptome sequencing, using pretransplant peripheral blood, algorithm reported as a risk score for early acute rejection	Crosswalk to 81542: 0 Gapfill: 12 Abstain: 0
72	36	0320U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Transplant renal early acute rejection Specimen: POST-transplant blood Analyte: RNA expression by SELECT transcriptome Type of code: RNA/transcriptome expression	Nephrology (renal transplant), RNA expression by select transcriptome sequencing, using posttransplant peripheral blood, algorithm reported as a risk score for acute cellular rejection	Crosswalk to 81542: 0 Gapfill: 12 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
73	30	0314U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology cutaneous melanoma diagnosis Specimen: FFPE Analyte: mRNA gene expression Indication: suspicious 'mole' biopsy is indeterminant by standard microscopy. A gene expression profiling test is ordered to establish the	Oncology (cutaneous melanoma), mRNA gene expression profiling by RT-PCR of 35 genes (32 content and 3 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical result (ie, benign, intermediate, malignant)	Crosswalk to 81529: 8 Crosswalk to 0090U: 4 Gapfill: 0 Abstain: 0
74	31	0315U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology cutaneous SCC localized or distant risk Specimen: FFPE Analyte: mRNA gene expression Indication: Biopsy of a suspicious 'lesion' on scalp determined to be invasive cutaneous squamous cell carcinoma. A gene expression profiling	Oncology (cutaneous squamous cell carcinoma), mRNA gene expression profiling by RT-PCR of 40 genes (34 content and 6 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical risk result (ie, Class 1, Class 2A, Class 2B)	Crosswalk to 81529: 7 Gapfill: 5 Abstain: 0
75	12	0296U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology oral/oropharyngeal diagnosis Specimen: saliva Analyte: mRNA Indication: patients with smoking use and/or ≥ 50 y.o. submit saliva sample to assess oral cancer risk	Oncology (oral and/or oropharyngeal cancer), gene expression profiling by RNA sequencing at least 20 molecular features (eg, human and/or microbial mRNA), saliva, algorithm reported as positive or negative for signature associated with malignancy	Crosswalk to 0170U: 8 Gapfill: 4 Abstain: 0
76	58	0245U	Reconsideration	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology thyroid risk Specimen: nodule FNA Analyte: DNA and RNA Indication: For FNA (+) for Bethesda III or IV (III: follicular lesion of undetermined significance (FLUS) or an atypia of undetermined	Oncology (thyroid), mutation analysis of 10 genes and 37 RNA fusions and expression of 4 mRNA markers using next-generation sequencing, fine needle aspirate, report includes associated risk of malignancy expressed as a percentage)	Crosswalk to 81455: 4 Gapfill: 8 Abstain: 0
77	29	0313U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology pancreas neoplasia diagnosis Specimen: liquid, pancreatic cyst fluid Analyte: DNA and mRNA Indication: 0313U is a diagnostic test for pancreatic cysts Type of code: Genomic sequence analysis and gene expression w	Oncology (pancreas), DNA and mRNA next-generation sequencing analysis of 74 genes and analysis of CEA (CEACAM5) gene expression, pancreatic cyst fluid, algorithm reported as a categorical result (ie, negative, low probability of neoplasia or positive, high probability of neoplasia)	Crosswalk to 0026U: 12 Gapfill: 0 Abstain: 0
78	60	0324U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology ovarian therapy optimization Specimen: newly retrieved tumor tissue Analyte: tumor cell growth Indication: To determine tumor cell viability when exposed in a culture to specific chemotherapeuthic agents outlined in code descriptor.	Oncology (ovarian), spheroid cell culture, 4-drug panel (carboplatin, doxorubicin, gemcitabine, paclitaxel), tumor chemotherapy response prediction for each drug	Crosswalk to 0248U: 7 Gapfill: 4 Abstain: 1
79	61	0325U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology ovarian therapy optimization Specimen: newly retrieved tumor tissue Analyte: tumor cell growth Indication: To determine tumor cell viability when exposed in a culture to specific chemotherapeuthic agents outlined in code descriptor.	Oncology (ovarian), spheroid cell culture, poly (ADP-ribose) polymerase (PARP) inhibitors (niraparib, olaparib, rucaparib, velparib), tumor response prediction for each drug	Crosswalk to 0248U: 8 Gapfill: 3 Abstain: 1
80	83	0X33U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score THERAPY	Oncology pan-tumor therapy response Specimen: blood Analyte: DNA Indication: to assess if metastatic urothelial cancer has a response to anti-PD-L1 therapy.	Oncology (pan-tumor), genetic profiling of 8 DNA-regulatory (epigenetic) markers by quantitative polymerase chain reaction (qPCR), whole blood, reported as a high or low probability of responding to immune checkpoint–inhibitor therapy	Gapfill: 12 Abstain: 0
81	84	0X34U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Oncology liver surveillance Specimen: blood Analyte: cell free DNA + 3 proteins Indication: For scenarios when there's a clinical suspicion of prostate cancer. 0x44U is to determine presence or absence of molecular evidence	Oncology (liver), surveillance for hepatocellular carcinoma (HCC) in high-risk patients, analysis of methylation patterns on circulating cell-free DNA (cfDNA) plus measurement of serum of AFP/AFP-L3 and oncoprotein des-gamma-carboxy-prothrombin (DCP), algorithm reported as normal or abnormal result	Crosswalk to 81420 + 82107 +83951: 0 Gapfill: 12 Abstain: 0
82	94	0X44U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score (darkest highlight)	Oncology prostate Specimen: urine Analyte: exosome Indication: For scenarios when there's a clinical suspicion of prostate cancer. 0x44U is to determine presence or absence of molecular evidence	Oncology (prostate), exosome-based analysis of 442 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RT-qPCR), urine, reported as molecular evidence of no-, low-, intermediate- or high- risk prostate of cancer	Crosswalk to 0005U: 8 Gapfill: 4 Abstain: 0
83	38	0322U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score/ Chemistry	Neurology autism spectrum disorder Specimen: plasma Analyte: multiple enzymes, proteins, hormones Type of code: Chemistry LC-MS/MS	Neurology (autism spectrum disorder [ASD]), quantitative measurements of 14 acyl carnitines and microbiome-derived metabolites, liquid chromatography with tandem mass spectrometry (LC-MS/MS), plasma, results reported as negative or positive for risk of metabolic subtypes associated with ASD	Crosswalk to 0063U: 7 Gapfill: 5 Abstain: 0
84	64	0328U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Chemistry LC-MS/MS, Toxicology	Drug assay, definitive, 120 or more drugs and metabolites, urine, quantitative liquid chromatography with tandem mass spectrometry (LC-MS/MS), includes specimen validity and algorithmic analysis describing drug or metabolite and presence or absence of risks for a significant patient adverse event, per date of service	Crosswalk to 0143U: 5 Crosswalk to 0150U: 1 Gapfill 6 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
85	102	0X53U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score	Specimen: blood (serum) Analyte: proteins Indication: to determine risk for having bacterial or viral infection Type of code: chemistry with algorithm	Infectious disease (bacterial or viral), biochemical assays, tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), interferon gamma-induced protein-10 (IP-10), and C-reactive protein, serum, algorithm reported as likelihood of bacterial infection	Crosswalk to 81500: 10 Gapfill: 1 Abstain: 1
86	93	0X43U	PLA	Tests with algorithm in code descriptor to report risk/likelihood/predictive score ELECTROCHEMILUMINESCENT IMMUNOASSAY (ECLIA) ALGORITHM	Specimen: blood (serum) Analyte: PROTEIN BIOMARKER Indication: Annual surveillance for pancreatic cancer given a strong family history. Type: multiplex electrochemiluminescent immunoassay	Oncology (pancreatic cancer), multiplex immunoassay of C5, C4, cystatin C, factor B, osteoprotegerin (OPG), gelsolin, IGFBP3, CA125 and multiplex electrochemiluminescent immunoassay (ECLIA) for CA19-9, serum, diagnostic algorithm reported qualitatively as positive, negative, or borderline	Crosswalk to 81503: 10 Crosswalk to 81490: 1 Gapfill: 1 Abstain: 0
87	28	0312U	PLA	Immunology ELISA	Immunology Specimen: blood or serum Analyte: Antibody biomarkers Indication: SLE Type of code: ELISA, FC, IIF	Autoimmune diseases (eg, systemic lupus erythematosus [SLE]), analysis of 8 IgG autoantibodies and 2 cell-bound complement activation products using enzyme-linked immunosorbent immunoassay (ELISA), flow cytometry and indirect immunofluorescence, serum, or plasma and whole blood, individual components reported along with an algorithmic SLE-likelihood assessment	Crosswalk to 0062U: 9 Crosswalk to 0003U: 3 Abstain: 0
88	42	86015	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody Indication: assist with diagnosis of autoimmune pathologies (autoimmune hepatitis) Type: immunoassay	Actin (smooth muscle) antibody (ASMA), each	Crosswalk to 86146: 9 Crosswalk to 83516: 2 Gapfill: 1 Abstain: 0
89	43	86036	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody Indication: assist with diagnosis of autoimmune pathologies Type: immunoassay (fluorescent)	ANCA screen, each	Crosswalk to 86146: 10 Crosswalk to 84586: 0 Crosswalk to 86255: 2 Gapfill: 0 Abstain: 0
90	44	86037	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody Indication: assist with diagnosis of autoimmune pathologies Type: immunoassay (fluorescent)	ANCA titer	Crosswalk to 86146: 8 Crosswalk to 86256: 4 Gapfill: 0 Abstain: 0
91	45	86051	Reconsideration	Immunology	Specimen: blood (serum) Analyte: neuromyelitis optica antibody Indication: diagnosis of neuromyelitis optica Type: ELISA	Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA)	Crosswalk to 86146: 11 Crosswalk to 83516: 1 Gapfill: 0 Abstain: 0
92	46	86052	Reconsideration	Immunology	Specimen: blood (serum) Analyte: neuromyelitis optica antibody Indication: diagnosis of neuromyelitis optica Type: cell-based immunofluorescence assay	Aquaporin-4 (neuromyelitis optica [NMO]) antibody; cell-based immunofluorescence assay (CBA), each	Crosswalk to 86341: 12 Crosswalk to 86255: 0 Gapfill: 0 Abstain: 0
93	47	86053	Reconsideration	Immunology	Specimen: blood (serum) Analyte: neuromyelitis optica antibody Indication: diagnosis of neuromyelitis optica Type: flow cytometry (fluorescence-activated cell sorting)	Aquaporin-4, flow cytometry (ie, fluorescence-activated cell sorting [FACS])	Crosswalk to 86367: 12 Crosswalk to 86255: 0 Gapfill: 0 Abstain: 0
94	48	86231	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody Indication: assist with diagnosis of Celiac disease Type: immunofluorescence assay	Endomysial antibody	Crosswalk to 86038 x 2: 5 Crosswalk to 86038: 3 Gapfill: 4 Abstain: 0
95	49	86258	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody Indication: assist with diagnosis of Celiac disease Type: ELISA	Gliadin (deamidated) (DGP) antibody	Crosswalk to 86147: 11 Crosswalk to 83516: 1 Gapfill: 0 Abstain: 0
96	50	86362	Reconsideration	Immunology	Specimen: blood (serum) Analyte: MOG antibody Indication: assist with diagnosis of MOG antibody disease Type: cell-based immunofluorescence assay	MOG IgG1, cell-based immunofluorescence assay	Crosswalk to 86357: 12 Gapfill: 0 Abstain: 0

FACA Mtg. Item	ALM Code List Item #	Code #	Code Type	Category	Subcategory for order of codes during FACA Meeting	Long Code Descriptor	Panel Recommendation
97	51	86363	Reconsideration	Immunology	Specimen: blood (serum) Analyte: MOG antibody Indication: assist with diagnosis of MOG antibody disease Type: flow-cytometry (fluorescence-activated cell sorting)	MOG IgG1, flow cytometry (ie, fluorescence-activated cell sorting [FACS]	Crosswalk to 86367: 12 Crosswalk to 86255: 0 Gapfill: 0 Abstain: 0
98	52	86364	Reconsideration	Immunology	Specimen: blood (serum) Analyte: tTG antibody Indication: assist with diagnosis of Celiac disease Type: ELISA	Tissue transglutaminase, each immunoglobulin	Crosswalk 86147: 11 Crosswalk 83516: 1 Gapfill: 0 Abstain: 0
99	53	86409	Reconsideration	Immunology	Specimen: blood (serum) Analyte: neutralizing antibody to SARS-CoV-2 Indication: assess eligibilty for conv plasma donation Type: cell function luminescence assay	Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer	Crosswalk to 86352: 10 Gapfill: 2 Abstain: 0
100	54	86413	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody to SARS-CoV-2 Indication: assess acquired immunity to SARS-CoV-2 Type: immunoassay (? Type)	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) antibody, quantitative	Gapfill: 12 Abstain: 0
101	55	86596	Reconsideration	Immunology	Specimen: blood (serum) Analyte: antibody voltage gated calcium channel Indication: assist with diagnosis of Lambert-Eaton myasthenic syndrome Type: immunoassay (RIA)	Voltage gated calcium channel antibody, each	Crosswalk to 84586: 11 Crosswalk to 83519: 1 Abstain: 0
102	56	87428	Reconsideration	Microbiology	Specimen: blood (serum) Analyte: protein biomarker expression plasma cells Indication: diagnosis of plasma cell disorders and myeloma Type: (?immunomagnetic selection, immunofluorescence staining, morph characterization, counting?)	Infectious agent antigen detection by immunoassay technique (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], fluorescence immunoassay [FIA], immunochemiluminometric assay [IMCA]), qualitative or semiquantitative; severe acute respiratory syndrome coronavirus (eg, SARS-CoV, SARS-CoV-2 [COVID-19]) and influenza virus types A and	Crosswalk to (87400 x 2) + 87426: 9 Crosswalk to 87430 +87400: 0 Crosswalk to 87430 + (87400 x 2): 1 Gapfill: 0 Abstain: 2
103	87	0X37U	PLA	Immunology/ IMMUNOMAGNETIC IMMUNOFLUORESCENT	Specimen: blood (serum) Analyte: protein biomarker expression plasma cells Indication: diagnosis of plasma cell disorders and myeloma Type: (?immunomagnetic selection, immunofluorescence staining, morph characterization, counting?)	Oncology (plasma cell disorders and myeloma), circulating plasma cell immunologic selection, identification, morphological characterization, and enumeration of plasma cells based on differential CD138, CD38, CD19, and CD45 protein biomarker expression, peripheral blood	Gapfill: 12 Abstain: 0
104	89	0X39U	PLA	Immunology/ IMMUNOMAGNETIC IMMUNOFLUORESCENT	Specimen: blood (serum) Analyte: PROTEIN BIOMARKER Indication: to evaluate CTC HER2 status in pts w triple negative breast CA not responsive to standard chemotherapy w multiple lung lesions inaccessible to biopsy	Oncology (solid tumor), circulating tumor cell selection, identification, morphological characterization, detection and enumeration based on differential EpCAM, cytokeratins 8, 18, and 19, and CD45 protein biomarkers, and quantification of HER2 protein biomarker–expressing cells, peripheral blood	Gapfill:11 Abstain: 1
105	105	0X56U	PLA	Microbiology		Human papilloma virus (HPV), high-risk types (ie, 16, 18, 31, 33, 45, 52 and 58) qualitative mRNA expression of E6/E7 by quantitative polymerase chain reaction (qPCR)	Crosswalk to 87624: 12 Gapfill: 0 Abstain: 0